

Always

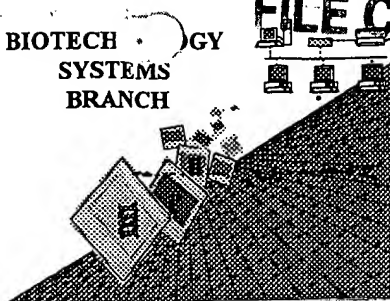
RAW SEQUENCE LISTING ERROR REPORT

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SYSTEMS
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TECH CENTER 600/2900



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/423,035
Source: 1635
Date Processed by STIC: 11/16/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/423,035

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1635

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/423,035

DATE: 11/16/2000
 TIME: 12:11:55

Input Set : A:\Scr21901.app
 Output Set: N:\CRF3\11162000\I423035.raw

see
 PP. 5, 2
 #8/seq.
 listing
 (error)

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: Joyce, Gerald F.
 4 Breaker, Ronald R.
 6 <120> TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
 8 <130> FILE REFERENCE: SCR2190S
 10 <140> CURRENT APPLICATION NUMBER: 09/423,035
 11 <141> CURRENT FILING DATE: 2000-01-13
 13 <150> PRIOR APPLICATION NUMBER: PCT/US98/08677
 14 <151> PRIOR FILING DATE: 1998-04-29
 16 <150> PRIOR APPLICATION NUMBER: 60/045,228
 17 <151> PRIOR FILING DATE: 1997-04-29
 19 <160> NUMBER OF SEQ ID NOS: 131
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 15
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Description of Artificial Sequence: 3' terminal
 30 sequence
 32 <400> SEQUENCE: 1
 33 cggtaaagctt ggcac 15
 36 <210> SEQ ID NO: 2
 37 <211> LENGTH: 20
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Artificial Sequence
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: The N
 43 at position 8 is adenosine ribonucleotide.
 45 <220> FEATURE:
 46 <223> OTHER INFORMATION: Description of Artificial Sequence: substrate
 48 <400> SEQUENCE: 2
 49 tcactatnag gaagagatgg 20
 52 <210> SEQ ID NO: 3
 53 <211> LENGTH: 38
 54 <212> TYPE: DNA
 55 <213> ORGANISM: Artificial Sequence
 57 <220> FEATURE:
 58 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
 60 <400> SEQUENCE: 3
 61 acacatctct gaagtagcgc cgccgtatag tgacgcta 38
 64 <210> SEQ ID NO: 4
 65 <211> LENGTH: 80
 66 <212> TYPE: DNA
 67 <213> ORGANISM: Artificial Sequence
 69 <220> FEATURE:
 70 <223> OTHER INFORMATION: Description of Artificial Sequence: oligomer
 72 <400> SEQUENCE: 4

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/423,035

DATE: 11/16/2000

TIME: 12:11:55

Input Set : A:\Scr21901.app

Output Set: N:\CRF3\11162000\I423035.raw

*see item 10 on Enw
Summary
Sheet*

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W--> 73 gtgccaagct tacg[nnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn] 60
W--> 74 [nnnnn]tcgc catctcttcc 80
77 <210> SEQ ID NO: 5
78 <211> LENGTH: 28
79 <212> TYPE: DNA
80 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
83 <223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: The n
84 at position 28 is adenosine ribonucleotide.
86 <220> FEATURE:
87 <221> NAME/KEY: misc_feature
88 <222> LOCATION: (28)
89 <223> OTHER INFORMATION: 2'3' cyclic phosphate.
91 <220> FEATURE:
92 <223> OTHER INFORMATION: Description of Artificial Sequence: cleavage
93 produce
95 <400> SEQUENCE: 5
96 gggacgaatt ctaatacgac tcactatn 28
99 <210> SEQ ID NO: 6
100 <211> LENGTH: 28
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: The n
106 at position 28 is adenosine ribonucleotide.
108 <220> FEATURE:
109 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
111 <400> SEQUENCE: 6
112 gggacgaatt ctaatacgac tcactatn. 28
115 <210> SEQ ID NO: 7
116 <211> LENGTH: 19
117 <212> TYPE: DNA
118 <213> ORGANISM: Artificial Sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: The n
122 at position 8 is adenosine ribonucleotide.
124 <220> FEATURE:
125 <223> OTHER INFORMATION: Description of Artificial Sequence: substrate
127 <400> SEQUENCE: 7
128 tcactatn[gg aagagatgg] 19
131 <210> SEQ ID NO: 8
132 <211> LENGTH: 8
133 <212> TYPE: DNA
134 <213> ORGANISM: Artificial Sequence
136 <220> FEATURE:
137 <221> NAME/KEY: misc_feature
138 <222> LOCATION: (8)
139 <223> OTHER INFORMATION: The n at position 8 is adenosine nucleotide.
141 <220> FEATURE:

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RAW SEQUENCE LISTING DATE: 11/16/2000
 PATENT APPLICATION: US/09/423,035 TIME: 12:11:55

Input Set : A:\Scr21901.app
 Output Set: N:\CRF3\11162000\I423035.raw

142 <223> OTHER INFORMATION: Description of Artificial Sequence: template
 144 <400> SEQUENCE: 8
 145 ~~tcactatn~~ 8
 148 <210> SEQ ID NO: 9
 149 <211> LENGTH: 30
 150 <212> TYPE: DNA
 151 <213> ORGANISM: Artificial Sequence
 153 <220> FEATURE:
 154 <223> OTHER INFORMATION: Description of Artificial Sequence: template
 156 <400> SEQUENCE: 9
 157 ccactctcttc ctatagtgag tccggctgca 30
 160 <210> SEQ ID NO: 10
 161 <211> LENGTH: 15
 162 <212> TYPE: DNA
 163 <213> ORGANISM: Artificial Sequence
 165 <220> FEATURE:
 166 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
 168 <400> SEQUENCE: 10
 169 gtgccaaagct taccg 15
 172 <210> SEQ ID NO: 11
 173 <211> LENGTH: 43
 174 <212> TYPE: DNA
 175 <213> ORGANISM: Artificial Sequence
 177 <220> FEATURE:
 178 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
 180 <400> SEQUENCE: 11
 181 ctgcagaatt ctaatacgac tcactatagg aagagatggc gac 43
 184 <210> SEQ ID NO: 12
 185 <211> LENGTH: 19
 186 <212> TYPE: DNA
 187 <213> ORGANISM: Artificial Sequence
 189 <220> FEATURE:
 190 <223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: The n
 191 at position 8 is adenosine ribonucleotide.
 193 <220> FEATURE:
 194 <223> OTHER INFORMATION: Description of Artificial Sequence: substrate
 196 <400> SEQUENCE: 12
 197 ~~tcactatn~~ggg aagagatgg 19
 200 ~~tcactatn~~ggg aagagatgg
 201 <210> SEQ ID NO: 13
 202 <211> LENGTH: 43
 203 <212> TYPE: DNA
 204 <213> ORGANISM: Artificial Sequence
 205 <220> FEATURE:
 206 <223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: The n
 207 at position 28 is adenosine ribonucleotide.
 209 <220> FEATURE:
 210 <223> OTHER INFORMATION: Description of Artificial Sequence: fixed
 211 substrate
 213 <400> SEQUENCE: 13

RAW SEQUENCE LISTING DATE: 11/16/2000
 PATENT APPLICATION: US/09/423,035 TIME: 12:11:55

Input Set : A:\Scr21901.app
 Output Set: N:\CRF3\11162000\I423035.raw

214 gggacgaatt ctaatacgac tcactatn~~gg~~ aagagatggc gac 43
 217 <210> SEQ ID NO: 14
 218 <211> LENGTH: 50
 219 <212> TYPE: DNA
 220 <213> ORGANISM: Artificial Sequence
 222 <220> FEATURE:
 223 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
 224 domain
 226 <400> SEQUENCE: 14
 227 tcacacatct ctgaagtagc gccgccgtat gtgacgctag gggttcgcct 50
 230 <210> SEQ ID NO: 15
 231 <211> LENGTH: 50
 232 <212> TYPE: DNA
 233 <213> ORGANISM: Artificial Sequence
 235 <220> FEATURE:
 236 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
 237 domain
 239 <400> SEQUENCE: 15
 240 ggggggaacg ccgtaacaag ctctgaacta gcggttcgca tatagtcgta 50
 243 <210> SEQ ID NO: 16
 244 <211> LENGTH: 50
 245 <212> TYPE: DNA
 246 <213> ORGANISM: Artificial Sequence
 248 <220> FEATURE:
 249 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
 250 domain
 252 <400> SEQUENCE: 16
 253 cgggactccg tagcccatcg ctttttgcag cgtcaacgaa tagcgtatta 50
 256 <210> SEQ ID NO: 17
 257 <211> LENGTH: 50
 258 <212> TYPE: DNA
 259 <213> ORGANISM: Artificial Sequence
 261 <220> FEATURE:
 262 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
 263 domain
 265 <400> SEQUENCE: 17
 266 ccaccatgtc ttctcgagcc gaaccgatag ttacgtcata cctcccgat 50
 269 <210> SEQ ID NO: 18
 270 <211> LENGTH: 50
 271 <212> TYPE: DNA
 272 <213> ORGANISM: Artificial Sequence
 274 <220> FEATURE:
 275 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
 276 domain
 278 <400> SEQUENCE: 18
 279 gccagattgc tgctaccagc ggtacgaaat agtgaagtgt tcgtgactat 50
 282 <210> SEQ ID NO: 19
 283 <211> LENGTH: 50
 284 <212> TYPE: DNA

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/423,035
 DATE: 11/16/2000
 TIME: 12:11:55

Input Set : A:\Scr21901.app
 Output Set: N:\CRF3\11162000\I423035.raw

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285 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:
288 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
289     domain
291 <400> SEQUENCE: 19
292 ataggccatg ctttgctag cggcaccgta tagtgtacct gcccttatcg           50
295 <210> SEQ ID NO: 20
296 <211> LENGTH: 50
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
302     domain
304 <400> SEQUENCE: 20
305 tctgctctcc tctattctag cagtgcagcg aaatatgtcg aatagtcggg           50
308 <210> SEQ ID NO: 21
309 <211> LENGTH: 50
310 <212> TYPE: DNA
311 <213> ORGANISM: Artificial Sequence
313 <220> FEATURE:
314 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
315     domain
317 <400> SEQUENCE: 21
318 ttgcccagca tagtcggcag acgtgggtgtt agcgacacga taggcccggt           50
321 <210> SEQ ID NO: 22
322 <211> LENGTH: 50
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA enzyme
328     domain
330 <400> SEQUENCE: 22
331 ttgctagctc ggctgaactt ctgtagcgca accgaaatag tgaggcttga           50
334 <210> SEQ ID NO: 23
335 <211> LENGTH: 107
336 <212> TYPE: DNA
337 <213> ORGANISM: Artificial Sequence
339 <220> FEATURE:
340 <223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule: The n
341     at position 28 is adenosine ribonucleotide.
343 <220> FEATURE:
344 <223> OTHER INFORMATION: Description of Artificial Sequence: oligomer
346 <400> SEQUENCE: 23
W--> 347 gggacgaatt ctaatacgac tcactatngg aagagatggc gacatctcnn nnnnnnnnnn 60
W--> 348 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn gacggtaagc ttggcac 107
351 <210> SEQ ID NO: 24
352 <211> LENGTH: 49
353 <212> TYPE: DNA
354 <213> ORGANISM: Artificial Sequence

```

*Per 1.823 of new
 Sequence Rules, all
 n's must be explained
 in*

*<220>-<223>
 section'*

fyi!

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/423,035

DATE: 11/16/2000

TIME: 12:11:56

Input Set : A:\Scr21901.app

Output Set: N:\CRF3\11162000\I423035.raw

L:49 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:49 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:49 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:73 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:73 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:73 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:74 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:74 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
M:340 Repeated in SeqNo=4
L:96 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:112 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:112 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:112 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:128 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:128 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:128 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
L:145 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:197 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:197 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:197 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
L:214 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:214 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:214 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
L:347 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:347 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:347 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23
L:348 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:348 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
M:340 Repeated in SeqNo=23
L:683 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:50
L:683 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:50
L:683 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:50
L:684 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:50
L:684 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:50
M:340 Repeated in SeqNo=50
L:701 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:51
L:701 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:51
L:701 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:51
L:702 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:51
L:702 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:51
M:340 Repeated in SeqNo=51
L:1546 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:123